CLAIMS

1. An isolated and purified protein having an amino acid sequence which is at least 85% identical to an amino acid sequence encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18, wherein percent identity is determined using a Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 1.

2. The isolated and purified protein of claim 1 which is at least 85% identical to the amino acid sequence shown in SEQ ID NO:19.

3. The isolated and purified protein of claim 1 which comprises an amino acid sequence encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18.

4. The isolated and purified protein of claim 2 which comprises the amino acid sequence shown in SEQ ID NO:19.

5. An isolated and purified polypeptide which consists of at least 8 contiguous amino acids of a protein having an amino acid sequence encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18.

6. The isolated and purified polypeptide of claim 5 which consists of at least 8 contiguous amino acids of SEQ ID NO:19.

7. The isolated polypeptide of claim 6 which is selected from the group consisting of at least amino acids 461-489 of SEQ ID NO:19, at least amino acids 106-115 of SEQ ID NO:19, at least amino acids 297-306 of SEQ ID NO:19, and at least amino acids 8-20 of SEQ ID NO:19.

8. A fusion protein which comprises a first protein segment and a second protein segment fused to each other by means of a peptide bond, wherein the first protein segment consists of at least 8 contiguous amino acids selected from an amino acid sequence encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18.

9. The fusion protein of claim 8 wherein the first protein segment consists of at least 8 contiguous amino acids selected from the amino acid sequence shown in

SEQ ID NO:19.

10. A preparation of antibodies which specifically bind to a protein with an amino acid sequence encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18.

11. A cDNA molecule which encodes an isolated and purified protein having an amino acid sequence which is at least 85% identical to an amino acid sequence encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-18, wherein percent identity is determined using a Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 1.

12. The cDNA molecule of claim 11 which encodes a protein having an amino acid sequence which is at least 85% identical to SEQ ID NO:19.

13. A cDNA molecule which encodes at least 8 contiguous amino acids of a protein encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18.

14. The cDNA molecule of claim 13 which encodes SEQ ID NO:19.

15. The cDNA molecule of claim 14 which comprises SEQ ID NO:18.

16. A cDNA molecule comprising at least 12 contiguous nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18.

17. A cDNA molecule which is at least 85% identical to a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18, wherein percent identity is determined using a Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 1.

18. The cDNA molecule of claim 17 which is at least 85% identical to the nucleotide sequence shown in SEQ ID NO:18.

19. An isolated and purified subgenomic polynucleotide comprising a nucleotide segment which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18 after washing with 0.2 X SSC at 65 °C.

20. The isolated and purified subgenomic polynucleotide of claim 19 wherein the nucleotide segment hybridizes to a nucleotide sequence as shown in SEQ ID NO:18.

21. A construct comprising:

a promoter; and

a polynucleotide segment encoding at least 8 contiguous amino acids of a protein encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18, wherein the polynucleotide segment is located downstream from the promoter, wherein transcription of the polynucleotide segment initiates at the promoter.

22. The construct of claim 21 wherein the protein comprises the amino acid sequence of SEQ ID NO:19.

23. A host cell comprising a construct which comprises:

a promoter and:

a polynucleotide segment encoding at least 8 contiguous amino acids of a protein encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18.

24. The host cell of claim 23 wherein the protein has the amino acid sequence shown in SEQ ID NO:19.

25. A recombinant host cell comprising a new transcription initiation unit, wherein the new transcription initiation unit comprises in 5' to 3' order:

(a) an exogenous regulatory sequence;

(b) an exogenous exon; and

(c) a splice donor site,

wherein the new transcription initiation unit is located upstream of a coding sequence of a gene, wherein the coding sequence comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18, wherein the exogenous regulatory sequence controls transcription of the coding sequence of the gene.

26. The recombinant host cell of claim 25 wherein the gene has the coding sequence shown in SEQ ID NO:18.

27. A polynucleotide probe comprising (a) at least 12 contiguous nucleotides selected from the group consisting of SEQ ID NOS:1-18 and (b) a detectable label.

28. The polynucleotide probe of claim 27 wherein the at least 12 contiguous nucleotides are selected from SEQ ID NO:18.

29. A method for identifying a metastatic tissue or metastatic potential of a tissue, comprising the step of:

measuring in a tissue sample an expression product of a gene comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-4, 6-13, and 15-18, wherein a tissue sample which expresses a product of a gene comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 4, 11, 16, 17, and 18 or which does not express a product of a gene comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:2, 3, 6, 7, 8, 9, 10, 12, 13, and 15 is identified as metastatic or as having metastatic potential.

30. The method of claim 29 wherein the tissue sample is selected from the group consisting of breast and colon tissue.

31. The method of claim 29 wherein the expression product is protein.

32. The method of claim 29 wherein the expression product is mRNA.

33. The method of claim 29 wherein the gene comprises the nucleotide sequence shown in SEQ ID NO:18.

34. A method of screening test compounds for the ability to suppress the metastatic potential of a tumor, comprising the steps of:

contacting a biological sample with a test compound; and

measuring in the biological sample the synthesis of a protein having an amino acid sequence encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-4, 6-13, and 15-18, wherein a test compound which decreases synthesis of a protein encoded by a polynucleotide comprising SEQ ID NOS:1, 4, 11, 16, 17, or 18 or which increases synthesis of a protein encoded by a polynucleotide comprising SEQ ID NOS:2, 3, 6, 7, 8, 9, 10, 12, 13, or 15 is identified as a potential agent for suppressing the metastatic potential of a tumor.

35. A method of predicting propensity for high-grade or low-grade metastatic spread of a colon tumor, comprising the steps of:

measuring in a colon tumor sample an expression product of a gene having a sequence selected from the group consisting of SEQ ID NOS:16 and 17, wherein a colon tumor sample which expresses the product of SEQ ID NO:16 is

categorized as having a high propensity to metastasize and a colon tumor sample which expresses the product of SEQ ID NO:17 is categorized as having a low propensity to metastasize.

36. A set of primers for amplifying at least a portion of a gene having a coding sequence selected from the group consisting of the nucleotide sequences shown in SEQ ID NOS:1-18.

37. The set of claim 36 wherein the gene has the coding sequence shown in SEQ ID NO:18.

38. The set of claim 37 wherein the primers are the nucleotide sequences shown in SEQ ID NOS:20 and 21.

39. A polynucleotide array comprising at least one single-stranded polynucleotide which comprises at least 12 contiguous nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-18.

40. The polynucleotide array of claim 40 wherein the nucleotide sequence is selected from the group consisting of SEQ ID NOS:1, 4, 11, 16, 17, and 18.

41. The polynucleotide array of claim 40 wherein the nucleotide sequence is selected from the group consisting of SEQ ID NOS:2, 3, 6, 7, 8, 9, 10, 12, 13, and 15.

42. A method of identifying a metastatic tissue or metastatic potential of a tissue, comprising the steps of:

contacting a tissue sample comprising single-stranded polynucleotide molecules with a polynucleotide array comprising at least one single-stranded polynucleotide probe, wherein the at least one single-stranded polynucleotide probe comprises at least 12 contiguous nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-4, 6-13, and 15-18, wherein the tissue sample is suspected of being metastatic or of having metastatic potential;

detecting double-stranded polynucleotides bound to the polynucleotide array, wherein detection of a double-stranded polynucleotide comprising contiguous nucleotides selected from the group consisting of SEQ ID NOS:1-4, 11, 16, 17, and 18 or lack of detection of a double-stranded polynucleotide comprising contiguous nucleotides selected from the group consisting of SEQ ID NOS:2, 3, 6, 7, 8, 9, 10, 12, 13, and 15 identifies the tissue sample as metastatic or of having metastatic potential.

43. The method of claim 42 wherein the tissue sample is a breast or colon sample.